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WO 00/11161

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SEQUENCE LISTING

<110> FUSO PHARMACEUTICAL INDUSTRIES, LTD.

<120> Novel Collectin

<130> 99P147W0

<150> JP 10-237611

<151> 1998-08-24

<160> 29

<210> 1

<211> 2024

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (670)..(1695)

<400> 1

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| gtcacgaatc | tgcagcaaga | taccagcgta  | ctccaggcca | atctgcagaa | ccaaatgtat | 60  |
| tctcataatg | tggtcatcat | gaacctcaac  | aacctgaacc | tgaccagggt | gcagcagagg | 120 |
| aacctcatca | cgaatctgca | gcggctgttg  | gatgacacaa | gccaggctat | ccagcgaatc | 180 |
| aagaacgact | ttcaaaatct | gcagcagggtt | tttcttcaag | ccaagaagga | cacggatgg  | 240 |
| ctgaaggaga | aagtgcagag | cttgcagacg  | ctggctgcc  | acaactctgc | gttggccaaa | 300 |
| gccaacaacg | acacccttgg | ggatatgaac  | agccagctca | actcattcac | aggtcagatg | 360 |

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|                         |                 |                 |             |             |            |      |
|-------------------------|-----------------|-----------------|-------------|-------------|------------|------|
| gagaacatca              | ccactatctc      | tcaagccaac      | gaggcagaacc | tgaaagaccc  | gcaggactt  | 420  |
| cacaaagatg              | cagagaatag      | aacagccatc      | aagttaacc   | aactggagga  | acgccttcag | 480  |
| ctctttgaga              | cggatattgt      | gaacatcatt      | agcaatatca  | gttacacagc  | ccaccacctg | 540  |
| cggacgcgta              | ccagcaatct      | aatgaagtc       | aggaccactt  | gcacagatac  | ccttacccaa | 600  |
| cacacagatg              | atctgacctc      | cttgaataat      | accctggcca  | acatccgtt   | ggattctgtt | 660  |
| tctctcagg               | atg caa caa     | gat ttg atg     | agg tcg agg | tta gac act | gaa gta    | 711  |
|                         | Met Gln Gln Asp | Leu Met Arg     | Ser Arg Leu | Asp Thr Glu | Val        |      |
| 1                       | 5               | 10              |             |             |            |      |
| gcc aac tta tca         | gtt att atg     | gaa gaa atg     | aag cta gta | gac tcc aag |            | 759  |
| Ala Asn Leu Ser Val Ile | Met Glu Glu     | Met Lys Leu Val | Asp Ser Lys |             |            |      |
| 15                      | 20              | 25              | 30          |             |            |      |
| cat ggt cag ctc atc     | aag aat ttt     | aca ata cta     | caa ggt cca | ccg ggc     |            | 807  |
| His Gly Gln Leu Ile     | Lys Asn Phe Thr | Ile Leu Gln Gly | Pro Pro Gly |             |            |      |
| 35                      | 40              | 45              |             |             |            |      |
| ccc agg ggt cca         | aga ggt gac     | aga gga tcc     | cag gga ccc | cct ggc cca |            | 855  |
| Pro Arg Gly Pro Arg     | Gly Asp Arg Gly | Ser Gln Gly     | Pro Pro Gly |             |            |      |
| 50                      | 55              | 60              |             |             |            |      |
| act ggc aac aag gga     | cag aaa gga     | gag aag ggg     | gag cct gga | cca cct     |            | 903  |
| Thr Gly Asn Lys Gly     | Gln Lys Gly     | Glu Lys Gly     | Glu Pro Gly | Pro Pro     |            |      |
| 65                      | 70              | 75              |             |             |            |      |
| ggc cct gcg ggt         | gag aga ggc cca | att gga cca     | gct ggt ccc | ccc gga     |            | 951  |
| Gly Pro Ala Gly         | Glu Arg Gly     | Pro Ile Gly     | Pro Ala Gly | Pro Pro Gly |            |      |
| 80                      | 85              | 90              |             |             |            |      |
| gag cgt ggc ggc         | aaa gga tct     | aaa ggc tcc     | cag ggc ccc | aaa ggc tcc |            | 999  |
| Glu Arg Gly             | Gly Lys Gly     | Ser Lys Gly     | Ser Gln Gly | Pro Lys Gly | Ser        |      |
| 95                      | 100             | 105             | 110         |             |            |      |
| cgt ggt tcc cct         | ggg aag ccc     | ggc cct         | cag ggc ccc | agt ggg gac | cca        | 1047 |
| Arg Gly Ser Pro         | Gly Lys Pro     | Gly Pro Gln     | Gly Pro Ser | Gly Asp     | Pro        |      |
| 115                     | 120             | 125             |             |             |            |      |

|   |      |     |     |
|---|------|-----|-----|
| ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc   | 1095 |     |     |
| Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly   |      |     |     |
| 130   | 135  | 140 |     |
| cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg   | 1143 |     |     |
| Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val   |      |     |     |
| 145   | 150  | 155 |     |
| cct gga cct cggtt gga ctg cca ggc ttg cct ggg gta cca ggc atg cca | 1191 |     |     |
| Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro   |      |     |     |
| 160   | 165  | 170 |     |
| ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg   | 1239 |     |     |
| Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val   |      |     |     |
| 175   | 180  | 185 | 190 |
| ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc   | 1287 |     |     |
| Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly   |      |     |     |
| 195   | 200  | 205 |     |
| tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca   | 1335 |     |     |
| Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser   |      |     |     |
| 210   | 215  | 220 |     |
| gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag   | 1383 |     |     |
| Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys   |      |     |     |
| 225   | 230  | 235 |     |
| tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata   | 1431 |     |     |
| Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile   |      |     |     |
| 240   | 245  | 250 |     |
| aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac   | 1479 |     |     |
| Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp   |      |     |     |
| 255   | 260  | 265 | 270 |
| tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac   | 1527 |     |     |
| Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp   |      |     |     |

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|  |     |     |      |
|--|-----|-----|------|
| 275  | 280 | 285 |      |
| tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat        |     |     | 1575 |
| Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His        |     |     |      |
| 290  | 295 | 300 |      |
| ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac        |     |     | 1623 |
| Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn        |     |     |      |
| 305  | 310 | 315 |      |
| gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg        |     |     | 1671 |
| Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg        |     |     |      |
| 320  | 325 | 330 |      |
| gag aca gta ctg tca tct gca tta taacggactg tcatggatc acatgagcaa        |     |     | 1725 |
| Glu Thr Val Leu Ser Ser Ala Leu  |     |     |      |
| 335  | 340 |     |      |
| atttttagct ctcaaaggca aaggacactc ctttctaatt gcatcacctt ctcatcagat      |     |     | 1785 |
| tgaaaaaaaaaaa aaaagcactg aaaaccaatt actgaaaaaaaaa aattgacagc tagtgtttt |     |     | 1845 |
| taccatccgt cattacccaa agacitggaa actaaaaatgt tccccagggt gataatgtga     |     |     | 1905 |
| ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt      |     |     | 1965 |
| atacaaattt atgtttccaa agtatggaac actccaatca gaaaaaggaa atcatcccg       |     |     | 2024 |

&lt;210&gt; 2

&lt;211&gt; 547

&lt;212&gt; PRT

&lt;213&gt; Homo Sapiens

&lt;220&gt;

&lt;223&gt; Deduced Amino Acid Sequence of Novel Collectin from Nucleotide Sequence.

&lt;400&gt; 2

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Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu  
1 5 10 15

Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val  
20 25 30

Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn  
35 40 45

Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys  
50 55 60

Glu Lys Val Gln Ser Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu  
65 70 75 80

Ala Lys Ala Asn Asn Asp Thr Leu Glu Asp Met Asn Ser Gln Leu Asn  
85 90 95

Ser Phe Thr Gly Gln Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn  
100 105 110

Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn  
115 120 125

Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu Arg Phe Gln Leu Phe  
130 135 140

Glu Thr Asp Ile Val Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His  
145 150 155 160

His Leu Arg Thr Leu Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys  
165 170 175

Thr Asp Thr Leu Thr Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn  
180 185 190

Thr Leu Ala Asn Ile Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln  
195 200 205

Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val  
210 215 220

Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile

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225                    230                    235                    240  
Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg  
245                    250                    255  
Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly  
260                    265                    270  
Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu  
275                    280                    285  
Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys  
290                    295                    300  
Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly  
305                    310                    315                    320  
Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro  
325                    330                    335  
Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln  
340                    345                    350  
Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly  
355                    360                    365  
Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro  
370                    375                    380  
Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln  
385                    390                    395                    400  
Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly Cys Pro Pro His Trp  
405                    410                    415  
Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile  
420                    425                    430  
Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val  
435                    440                    445  
Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val  
450                    455                    460

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Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn

465 470 475 480

Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys

485 490 495

Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro Gly Glu Asp

500 505 510

Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu

515 520 525

Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser

530 535 540

Ser Ala Leu

545

<210> 3

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Consensus Sequence of collectins Hybridizable with Novel Collectin.

<400> 3

Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn

1 5 10 15

Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe

20 25

<210> 4

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Reverse Primer for Screening a Novel Collectin.

<400> 4

caatctgatg agaaggatgat g

21

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Forward Primer for Screening a Novel Collectin.

<400> 5

acgaggggctt ggatgggaca t

21

<210> 6

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence of three collectins which were reported heretofore.

<400> 6

Glu Asp Cys Val Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro  
1 5 10 15  
Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe  
20 25

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> M13 Universal Primer Sequence for Sequencing.

<400> 7

cgacgttgta aaacgacggc cagt 24

<210> 8

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> M13 Reverse Primer Sequence for Sequencing.

<400> 8

caggaaaca gctatgac 17

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&lt;210&gt; 9

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sequence of a λgt11 Reverse Primer for Sequencing.

&lt;400&gt; 9

ttgacaccag accaactgg t aatg

24

&lt;210&gt; 10

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sequence of a λgt11 Forward Primer for Sequencing.

&lt;400&gt; 10

gg tggcgacg act cctggag cccg

24

&lt;210&gt; 11

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sequence of a Primer for Screening a Novel Collectin.

<400> 11

cgtgaaaatg aatggaaatg g

21

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Primer for Screening a Novel Collectin.

<400> 12

ttttatccat tgctgttcct c

21

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Primer for Sequencing a Novel Collectin.

<400> 13

ctggcagtcc ccgaggccca g

21

<210> 14

<211> 21

<212> DNA

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<213> Artificial Sequence

<220>

<223> Sequence of a Primer for Sequencing a Novel Collectin.

<400> 14

gctggtcccc ccggagagcg t

21

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a 1RC2 Primer for Cap Site Sequencing.

<400> 15

caaggtaacgc cacagcgtat g

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Synthetic TGPI Primer for Cap Site Sequencing.

<400> 16

tcttcagttt ccctaattcc

20

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a 2RC2 Primer for Cap Site Sequencing.

<400> 17

gtacgccaca gcgtatgatg c

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Synthetic TGP2 Primer for Cap Site Sequencing.

<400> 18

cattcttgac aaacttcata g

21

<210> 19

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Primer for Screening a Novel Collectin.

<400> 19

gaagacaagt cttcaactct tg

22

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Primer for Screening a Novel Collectin.

<400> 20

ctctgagtc t gtgaggccga tc

22

<210> 21

<211> 111

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Probe for Screening a Novel Collectin.

<400> 21

gaagacaagt ctccacatct tgttttcata aacactagag aggaacagca atggataaaa 60  
aaacagatgg tagggagaga gagccactgg atcgccctca cagactcaga g 111

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Forward Primer for Screening a Novel Collectin.

<400> 22

gtgccccctgg ccctgcagaa tg

22

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Reverse Primer for Screening a Novel Collectin.

<400> 23

gcatatcacc ctggggaaca ttttag

26

<210> 24

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Sense Primer for Screening  $\beta$ -Actin.

<400> 24

caagaga~~t~~gg ccacggctgc t

21

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of an Antisense Primer for Screening  $\beta$ -Actin.

<400> 25

tccttctgca tcctgtcggc a

21

<210> 26

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Sense Primer for Amplifying the Novel Collectin.

<400> 26

aaggaaaaaa gcggccgcat gcaacaagat ttgatgagg

39

<210> 27

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Reverse Primer for Amplifying the Novel Collectin.

<400> 27

gctcttagatt ataatgcaga tgacagttac

29

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Sense Primer for Amplifying the Nockout Gene.

<400> 28

atgcaacaag atttgatgag g

21

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of a Sense Primer for Amplifying the Nockout Gene.

<400> 29

cctaccgggt agaatttggacc

20